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INVENTOR: Nabil HANNA et al.  
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TITLE: RECOMBINANT ANTI-CD4 ANTIBODIES OR HUMAN THERAPY  
PILLSBURY WINTHROP LLP  
MCLEAN, VIRGINIA

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## Figure 1

M K H L W F F L L L V A A P R  
GAC ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCC CCC AGA

W V L S Q V Q L Q E A G P G L V  
TGG GTC TTG TCC CAG GTG CAG CTG CAG GAG GCG GGC CCA GGA CTG GTG  
+1 10

K P S E T L S L T C S V S G G S  
AAG CCT TCG GAG ACC CTG TCC CTC ACC TGC AGT GTC TCT GGT GGC TCC  
20

I S G D Y Y W F W I R Q S P G K  
ATC AGC GGT GAC TAT TAT TGG TTC TGG ATC CGC CAG TCC CCA GGG AAG  
30 40

G L E W I G Y I X G S G G G T N  
GGA CTG GAG TGG ATC GGC TAC ATC TAT GGC AGT GGT GGG GGC ACC AAT  
50 60

Y N P S L N N R V S I S I D T S  
TAC AAT CCC TCC CTC AAC AAT CGA GTC TCC ATT TCA ATA GAC ACG TCC  
70

K N L F S L K L R S V T A A D T  
AAG AAC CTC TTC TCC CTG AAA CTG AGG TCT GTG ACC GCC GCG GAC ACG  
80 90

A V Y Y C A S N I L K Y L H W L  
GCC GTC TAT TAC TGT GCG AGT AAT ATA TTG AAT TAT CTT CAC TGG TTA  
100

L Y W G Q G V L V T S S  
TTA TAC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC  
110 120



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## Figure 2

M A W A L L L G L L A H F T  
 ACC ATG GCC TGG GCT CTG CTG CTC GGC CTC CTT GCT CAC TTT ACA

+1 10  
 D S A A S Y E L S Q P R S V S V  
 GAC TCT GCG GCC TCC TAT GAG TTG AGT CAG CCT CGC TCA GTG TCC GTG

20  
 S P G Q T A G F T C G G D N V G  
 TCC CCA GGA CAG ACG GCC GGG TTC ACC TGT GGG GGA GAC AAC GTT GGA

30 40  
 R K S V Q W Y Q Q K P P Q A P V  
 AGG AAA AGT GTA CAG TGG TAC CAG CAG AAG CCA CCG CAG GCC CCT GTG

50 60  
 L V I Y A D S E R P S G I P A R  
 CTG GTC ATC TAT GCT GAC AGC GAA CGG CCC TCA GGG ATC CCT GCG CGA

70  
 F S G S N S G N T A T L T I S G  
 TTC TCT GGC TCC AAC TCA GGG AAC ACC GCC ACC CTG ACC ATC AGC GGG

80 90  
 V E A G D E A D Y Y C Q V W D S  
 GTC GAG GCC GGG GAT GAG GCT GAC TAT TAC TGT CAG GTG TGG GAC AGT

100  
 T A D H W V F G G G T R L T V L  
 ACT GCT GAT CAT TGG GTC TTC GGC GGA GGG ACC CGG CTG ACC GTC CTA

109  
 G  
 GGT



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**Figure 3**

Frame 1 Met Ala Trp Ala Leu Leu Leu Gly Leu Leu Ala His Phe Thr Asp Ser Ala Ala  
 ATG GCC TGG GCT CTG CTG CTC GGC CTC CTT GCT CAC TTT ACA GAC TCT GCG GCC  
 9 18 27 36 45 54

Ser Tyr Glu Leu Ser Gln Pro Arg Ser Val Ser Val Ser Pro Gly Gln Thr Ala Gly Phe Thr  
 TCC TAT GAG TTG AGT CAG CCT CGC TCA GTG TCC GTG TCC CCA GGA CAG ACG GCC GGG TTC ACC  
 66 75 84 93 102 111 120

Cys Gly Gly Asp Asn Val Gly Arg Lys Ser Val Gln Trp Tyr Gln Gln Lys Pro Pro Gin Ala  
 TGT GGG GGA GAC AAC GTT GGA AGG AAA AGT GTA CAG TGG TAC CAG CAG AAG CCA CCG CRG GCC  
 129 138 147 156 165 174 183

Pro Val Leu Val Ile Tyr Ala Asp Ser Glu Arg Pro Ser Gly Ile Pro Ala Arg Phe Ser Gly  
 CCT GTG CTG GTC ATC TAT GCT GAC AGC GAA CGG CCC TCA GGG ATC CCT GCG CGA TTC TCT GGC  
 192 201 210 219 228 237 246

Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Val Glu Ala Gly Asp Glu Ala Asp  
 TCC AAC TCA GGG AAC ACC GCC ACC ATC AGC GGG GTC GAG GCC GGG GAT GAG GCT GAC  
 255 264 273 282 291 300 309

Tyr Tyr Cys Gln Val Trp Asp Ser Thr Ala Asp His Trp Val Phe Gly Gly Gly Thr Arg Leu  
 TAT TAC TGT CAG GTG TGG GAC AGT ACT GCT GAT CAT TGG GTC TTC GGC GGA GGG ACC CGG CTG  
 318 327 336 345 354 363 372

Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu  
 ACC GTC CTA GGT CAG CCC AAG GCT GCC CCC TCG GTC ACT CTG TTC CCG CCC TCC TCT GAG GAG  
 381 390 399 408 417 426 435

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr  
 CTT CAA GCC AAC AAG GCC ACA CTG GTG TGT CTC ATA AGT GAC TTC TAC CCG GGA GCC GTG ACA  
 444 453 462 471 480 489 498

Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys  
 GTG GCC TGG AAG GCA GAT AGC AGC CCC GTC AAG GCG GGA GTG GAG ACC ACC ACA CCC TCC AAA  
 507 516 525 534 543 552 561

Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
 CAA AGC AAC AAC AAG TAC GCG GCC AGC AGC TAC CTG AGC CTG ACG CCT GAG CAG TGG AAG TCC  
 570 579 588 597 606 615 624

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro  
 CAC AGA AGC TAC AGC TGC CAG GTC ACG CAT GAA GGG AGC ACC GTG GAG AAG ACA GTG GCC CCT  
 633 642 651 660 669 678 687

Thr Glu Cys Ser TER  
 ACA GAA TGT TCA TGA



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## Figure 4a

Frame 1 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser  
 ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCC CCC AGA TGG GTC TTG TCC  
 9 18 27 36 45 54

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr  
 CAG GTG CAG CTG CAG GAG TCG GGC CCA GGA CTG GTG AAG CCT TCG GAG ACC CTG TCC CTC ACC  
 66 75 84 93 102 111 120

Cys Ser Val Ser Gly Gly Ser Ile Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro  
 TGC AGT GTC TCT GGT GGC TCC ATC AGC GGT GAC TAT TAT TGG TTC TGG ATC CGC CAG TCC CCA  
 129 138 147 156 165 174 183

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Thr Asn Tyr Asn Pro  
 GGG AAG GGA CTG GAG TGG ATC GGC TAC ATC TAT GGC AGT GGT GGG GGC ACC AAT TAC ATC CCC  
 192 201 210 219 228 237 246

Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys Asn Leu Phe Ser Leu Lys Leu  
 TCC CTC AAC AAT CGA GTC TCC ATT TCA ATA GAC ACG TCC AAG AAC CTC TTC TCC CTG AAA CTG  
 255 264 273 282 291 300 309

Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu  
 AGG TCT GTG ACC GCC GCG GAC ACG GCC GTC TAT TAC TGT GCG AGT AAT ATA TTG AAA TAT CTT  
 318 327 336 345 354 363 372

His Trp Leu Leu Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
 CAC TGG TTA TTA TAC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC TCA GCT AGC ACC AAG GGC  
 381 390 399 408 417 426 435

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly  
 CCA TCC GTC TTC CCC CTG GCG CCC TGC TCC AGG AGC ACC TCC GAG AGC ACA GCA GCC GGC CTG GGC  
 444 453 462 471 480 489 498

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr  
 TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG ACC  
 507 516 525 534 543 552 561

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
 AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG  
 570 579 588 597 606 615 624

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro  
 GTG ACC GTG CCC TCC AGC AGC TTG GGC ACG AAG ACC TAC ACC TGC AAC GTA GAT CAC AAG CCC  
 633 642 651 660 669 678 687

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro



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## Figure 4b

AGC AAC ACC AAG GTG GAC AAG AGA GTT GAG TCC AAA TAT GGT CCC CCA TGC CCA TCA TGC CCA						
696	705	714	723	732	741	750

Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu						
GCA CCT GAG TTC CTG GGG GGA CCA TCA GTC TTC CTG CCC CCA AAA CCC AAG GAC ACT CTC						
759	768	777	786	795	804	813

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu						
ATG ATC TCC CGG ACC CCT GAG GTC ACG TGC GTG GTG GTG GAC GTG AGC CAG GAA GAC CCC GAG						
822	831	840	849	858	867	876

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu						
GTC CAG TTC AAC TGG TAC GTG GAT GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG						
885	894	903	912	921	930	939

Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu						
GAG CAG TTC AAC ACG ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG						
948	957	966	975	984	993	1002

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr						
AAC GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GGC CTC CCG TCC TCC ATC GAG AAA ACC						
1011	1020	1029	1038	1047	1056	1065

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu						
ATC TCC AAA GCC AAA GGG CAG CCC CCA GAG CCA CAG GTG TAC ACC CTG CCC CCA TCC CAG GAG						
1074	1083	1092	1101	1110	1119	1128

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile						
GAG ATG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAC CCC AGC GAC ATC						
1137	1146	1155	1164	1173	1182	1191

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu						
GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG						
1200	1209	1218	1227	1236	1245	1254

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu						
GAC TCC GAC GGC TCC TTC CTC TAC AGC AGG CTA ACC GTG GAC AAG AGC AGG TGG CAG GAG						
1263	1272	1281	1290	1299	1308	1317

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser						
GGG AAT GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACA CAG AAG AGC						
1326	1335	1344	1353	1362	1371	1380

Leu Ser Leu Ser Leu Gly Lys TER						
CTC TCC CTG TCT CTG GGT AAA TGA						
1389	1398					

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## Figure 5a

Frame 1 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser  
ATG AAA CAC CTG TGG TTC CTC CTC CTG GTG GCA GCC CCC AGA TGG GTC TTG TCC  
9 18 27 36 45 54

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr  
CAG GTG CAG CTG CAG GAG TCG GGC CCA GGA CTG GTG AAG CCT TCG GAG ACC CTG TCC CTC ACC  
66 75 84 93 102 111 120

Cys Ser Val Ser Gly Gly Ser Ile Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro  
TGC AGT GTC TCT GGT GGC TCC ATC AGC GGT GAC TAT TAT TGG TTC TGG ATC CGC CAG TCC CCA  
129 138 147 156 165 174 183

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Thr Asn Tyr Asn Pro  
GGG AAG GGA CTG GAG TGG ATC GGC TAC ATC TAT GGC AGT GGT GGG GGC ACC AAT TAC AAT CCC  
192 201 210 219 228 237 246

Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys Asn Leu Phe Ser Leu Lys Leu  
TCC CTC AAC AAT CGA GTC TCC ATT TCA ATA GAC ACC TCC AAG AAC CTC TTC TCC CTG AAA CTG  
255 264 273 282 291 300 309

Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu  
AGG TCT GTG ACC GCC GCG GAC ACG GGC GTC TAT TAC TGT GCG AGT AAT ATA TTG AAA TAT CTT  
318 327 336 345 354 363 372

His Trp Leu Leu Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
CAC TGG TTA TTA TAC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC TCA GCT AGC ACC AAG GGG  
381 390 399 408 417 426 435

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly  
CCA TCC GTC TTC CCC CTG GCG CCC TGC TCC AGG AGC ACC TCC GAG AGC ACA GCC GCC CTG GGC  
444 453 462 471 480 489 498

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr  
TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG ACC  
507 516 525 534 543 552 561

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG  
570 579 588 597 606 615 624

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro  
GTG ACC GTG CCC TCC AGC AGC TTG GGC ACG AAG ACC TAC ACC TGC AAC GTA GAT CAC AAG CCC  
633 642 651 660 669 678 687

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro



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## Figure 5b

AGC AAC ACC AAG GTG GAC AAG AGA GTT GAG TCC AAA TAT GGT CCC CCA TGC CCA TCA TGC CCA
696            705            714            723            732            741            750

Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Pro Pro Lys Pro Lys Asp Thr Leu
GCA CCT GAG TTC GAG GGG GGA CCA TCA GTC TTC CTG CCC CCA AAA CCC AAG GAC ACT CTC
759            768            777            786            795            804            813

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
ATG ATC TCC CGG ACC CCT GAG GTC ACG TGC GTG GTG GAC GTG AGC CAG GAA GAC CCC GAG
822            831            840            849            858            867            876

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
GTC CAG TTC AAC TGG TAC GTG GAT GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG
885            894            903            912            921            930            939

Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
GAG CAG TTC AAC AGC ACG TAC CGT GTG GTC ACC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG
948            957            966            975            984            993            1002

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr
AAC GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GGC CTC CCG TCC ATC GAG AAA ACC
1011            1020            1029            1038            1047            1056            1065

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
ATC TCC AAA GCC AAA GGG CAG CCC CGA GAG CCA CAG GTG TAC ACC CTG CCC CCA TCC CAG GAG
1074            1083            1092            1101            1110            1119            1128

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
GAG ATG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAC CCC AGC GAC ATC
1137            1146            1155            1164            1173            1182            1191

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG
1200            1209            1218            1227            1236            1245            1254

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
GAC TCC GAC GGC TCC TTC CTC TAC AGC AGG CTA ACC GTG GAC AAG AGC AGG TGG CAG GAG
1263            1272            1281            1290            1299            1308            1317

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
GGG AAT GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC TAC ACA CAG AAG AGC
1326            1335            1344            1353            1362            1371            1380

Leu Ser Leu Ser Leu Gly Lys TER
CTC TCC CTG TCT CTG GGT AAA TGA
1389            1398



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## Figure 6a

Frame 1 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser  
 ATG AAA CAC CTG TGG TTC CTC CTC CTG GTG GCA GCC CCC AGA TGG GTC TTG TCC  
 9 18 27 36 45 54

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr  
 CAG GTG CAG CTG CAG GAG TCG GGC CCA GGA CTG GTG AAG CCT TCG GAG ACC CTG TCC CTC ACC  
 66 75 84 93 102 111 120

Cys Ser Val Ser Gly Gly Ser Ile Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro  
 TGC AGT GTC TCT GGT GGC TCC ATC AGC GGT GAC TAT TAT TGG TTC TGG ATC CGC CAG TCC CCA  
 129 138 147 156 165 174 183

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Thr Asn Tyr Asn Pro  
 GGG AAG GGA CTG GAG TGG ATC GGC TAC ATC TAT GGC AGT GGT GGG GGC ACC AAT TAC ATC CCC  
 192 201 210 219 228 237 246

Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys Asn Leu Phe Ser Leu Lys Leu  
 TCC CTC AAC AAT CGA GTC TCC ATT TCA ATA GAC ACG TCC AAG AAC CTC TTC TCC CTG AAA CTG  
 255 264 273 282 291 300 309

Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu  
 AGG TCT GTG ACC GCC GCG GAC ACG GCC GTC TAT TAC TGT GCG AGT AAT ATA TTG AAA TAT CTT  
 318 327 336 345 354 363 372

His Trp Leu Leu Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
 CAC TGG TTA TTA TAC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC TCA GCT AGC ACC AAG GGG  
 381 390 399 408 417 426 435

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly  
 CCA TCC GTC TTC CCC CTG GCG CCC TGC TCC AGG AGC ACC TCC GAG AGC ACA GCC CTG GGC  
 444 453 462 471 480 489 498

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr  
 TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG ACC  
 507 516 525 534 543 552 561

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
 AGC GCC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG  
 570 579 588 597 606 615 624

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro  
 GTG ACC GTG CCC TCC AGC AGC TTG GGC ACG AAG ACC TAC ACC TGC AAC GTA GAT CAC AGC CCC  
 633 642 651 660 669 678 687

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro



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## Figure 6b

AGC AAC ACC AAG GTG GAC AAG AGA GTT GAG TCC AAA TAT GGT CCC CCA TGC CCA CCA TGC CCA  
 696 705 714 723 732 741 750

Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
 GCA CCT GAG TTC GAG GGG GGA CCA TCA GTC TTC CTG TTC CCC CCA AAA CCC AAG GAC ACT CTC  
 759 768 777 786 795 804 813

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu  
 ATG ATC TCC CGG ACC CCT GAG GTC ACG TGC GTG GTG GAC GTG AGC CAG GAA GAC CCC GAG  
 822 831 840 849 858 867 876

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu  
 GTC CAG TTC AAC TGG TAC GTG GAT GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG  
 885 894 903 912 921 930 939

Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu  
 GAG CAG TTC AAC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG  
 948 957 966 975 984 993 1002

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr  
 AAC GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GGC CTC CCG TCC TCC ATC GAG AAA ACC  
 1011 1020 1029 1038 1047 1056 1065

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu  
 ATC TCC AAA GCC AAA GGG CAG CCC CGA GAG CCA CAG GTG TAC ACC CTG CCC CCA TCC CAG GAG  
 1074 1083 1092 1101 1110 1119 1128

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
 GAG ATG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAC CCC AGC GAC ATC  
 1137 1146 1155 1164 1173 1182 1191

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu  
 GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG  
 1200 1209 1218 1227 1236 1245 1254

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu  
 GAC TCC GAC GGC TCC TTC CTC TAC AGC AGG CTA ACC GTG GAC AAG AGC AGG TGG CAG GAG  
 1263 1272 1281 1290 1299 1308 1317

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
 GGG AAT GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACA CAG ARG AGC  
 1326 1335 1344 1353 1362 1371 1380

Leu Ser Leu Ser Leu Gly Lys TER  
 CTC TCC CTG TCT CTG GGT AAA TGA  
 1389 1398



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## Figure 7a

### Primers for the Amplification of Monkey Immunoglobulin Heavy Chain Variable Regions

#### 5' 'Sense' Primers

##### A. Human or Monkey heavy chain early leader sequence primers with *Sall* site

V<sub>H</sub>1 5' ACTAAGTCGACATGGACTGGACCTGG 3'

V<sub>H</sub>2 5' ACTAAGTCGACATGGACATACTTTGTTCCAC 3'

V<sub>H</sub>3 5' ACTAAGTCGACATGGAGTTGGGCTGAGC 3'

V<sub>H</sub>4 5' ACTAAGTCGACATGAAACACCTGTGGTTCTT 3'

V<sub>H</sub>5 5' ACTAAGTCGACATGGGGTCAACCGCCATCCT 3'

V<sub>H</sub>6 5' ACTAAGTCGACATGTCTGTCTCCTCCTCAT 3'

##### B. Human or Monkey heavy chain late leader sequence primers with *Mlu I* site

V<sub>H</sub>1 5' G GCA GCA GC(CT) ACG CGT GCC CAC TCC GAG GT 3' <sup>+1</sup>

V<sub>H</sub>2 5' G ACC GTC CCG ACG CGT GT(TC) TTG TCC CAG GT 3' <sup>+1</sup>

V<sub>H</sub>3 5' GCT ATT TTC ACG CGT GTC CAG TGT GAG 3' <sup>+1</sup>

V<sub>H</sub>4 5' GCG GCT CCC ACG CGT GTC CTG TCC CAG 3' <sup>+1</sup>

V<sub>H</sub>5 5' G GCT GTT CTC ACG CGT GTC TGT GCC GAG GT 3' <sup>+1</sup>



**Appn. No.: 09/612,914**  
**INVENTOR: Nabib HANNA et al.**  
**FILED: July 10, 2000**  
**ATTORNEY DOCKET: 037003-0275643**  
**IDEC REF. NO.: 1999-30-0019CP4C1**  
**TITLE: RECOMBINANT ANTI-CD4 ANTIBODIES OR HUMAN THERAPY**

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**Figure 7b**

### **C. Human or Monkey framework 1 sequence primers with *Xba* I site**

$V_H$ 1,3a,5	+1 CAGGTGCAGCT <u>GCTCGAGT</u> CTGG
$V_H$ 2	+1 CAGGTCAACT <u>TACTCGAGT</u> CTGG
$V_H$ 3b	+1 GAGGTGCAGCT <u>GCTCGAGT</u> CTGG
$V_H$ 4	+1 CAGGTGCAGCT <u>GCTCGAGT</u> CGGG
$V_H$ 6	+1 CAGGTACAGCT <u>GCTCGAGT</u> CAGG

### 3' 'Anti-Sense' Primers.

**A. Human or Monkey Heavy Chain Constant Region Primers Anti-Sense Strand with *Nhe* 1 site**

IgG<sub>1-4</sub>      +118      5' GGC GGA TGC GCT AGC TGA GGA GAC GG 3'  
+110  
 Nhe 1



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## Figure 7c

### Primers for the Amplification of Monkey Immunoglobulin Light Chain Variable Regions

#### 5' 'Sense' Primers

##### A. Human or Monkey kappa light chain early leader primers with *Bgl II* site

1. 5'ATCACAGATCTTCACCATGGTGTGCAGACCCAGGTC 3'
2. 5'ATCACAGATCTTCACCATGG(GA)G(AT)CCCC(TA)GC(TG)CAGCT 3'
3. 5'ATCACAGATCTTCACCATGGACATGAGGGTCCCCGCTCAG 3'
4. 5'ATCACAGATCTTCACCATGGACAC(GAC)AGGGCCCCCACTCAG 3'

##### B. Human or Monkey lambda light chain early leader primers with *Bgl II* site

1. 5'ATCACAGATCTTCACCATGCCCTGGGCTTGCTGCTCC 3'
2. 5'ATCACAGATCTTCACCATGCCCTGGCTCCACTACTTC 3'
3. 5'ATCACAGATCTTCACCATGACCTGCTCCCTCTCCTCC 3'
4. 5'ATCACAGATCTTCACCATGCCCTGGACTCCTCTCTTC 3'
5. 5'ATCACAGATCTTCACCATGACTGGACCCCACTCCTC 3'



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**Figure 7d**

### 3' 'Anti-Sense' Primers

**A. Human or Monkey kappa light chain constant region primer anti-sense strand with *Kpn* 1 and *BsiW*1 sites**

C<sub>kappa</sub> +108 5' CCG TTT GAT TTC CAG CTT GGT ACC TCC ACC GAA CGT 3'  
 Kpn 1  
 +112 5' TGC AGC ATC CGT ACG TTT GAT TTC CAG CTT 3'  
 BsiW1 +103

**B. Human or Monkey lambda light chain constant region primer anti-sense strand with *Kpn* I, *Hind* III and *Avr* II sites.**

**C<sub>Lambda</sub>**

+107 +99  
 5' ACC TAG GAC GGT AAG CTT GGT ACC TCC GCC 3'  
Hind III Kpn I

+107 +97  
5' ACC TAG GAC GGT CA(C/G) (C/G)TT GGT ACC TCC GCC GAA CAC 3'  
Kpn 1

<sup>+110</sup>  
 5' CTT GGG CTG ACC TAG GAC GGT CAG CCG 3'  
Avt II



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## Figure 8

### A. Heavy Chain Variable Region:

VH1	5'	CCATGGACTGGACCTGG 3'
VH2	5'	ATGGACATACTTGTCCAC 3'
VH3	5'	CCATGGAGTTGGGCTGAGC 3'
VH4	5'	ATGAAACACCTGTGGTTCTT 3'
VH5	5'	ATGGGGTCAACCGCCATCCT 3'
VH6	5'	ATGTCTGTCTCCTTCCTCAT 3'

### B. Heavy Chain Constant Region Anti-Sense Strand:

IgM	5'	T TGG GGC GGA TGC ACT 3' +119 +115
IgG <sub>1-4</sub>	5'	GA TGG GCC CTT GGT GGA 3' +119 +115

### C. Light Chain Variable Region:

Kappa	5'	G ATG ACC CAG TCT CCA (G/T)CC TC 3' +4 +10 -9
Lambda	5'	CTC A(C/T)T (T/C)(G/A)C TGC (A/C)CA GGG TCC 3' -3

### D. Light Chain Constant Region Anti-Sense Strands:

Kappa	5'	AA GAC AGA TGG TGC AGC CA 3' +115 +110
Lambda	5'	G GAA CAG AGT GAC CGA GGG G 3' +118 +112

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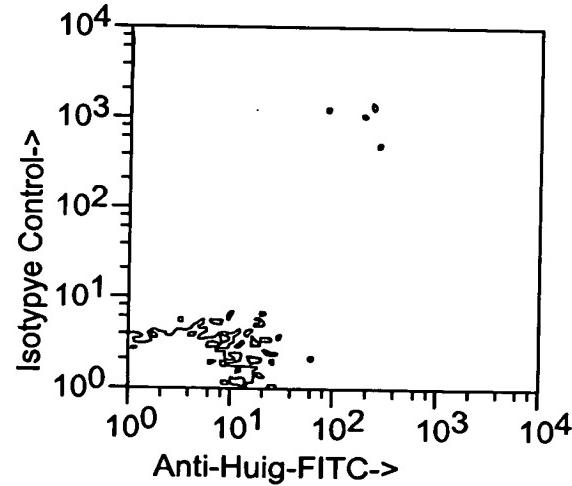
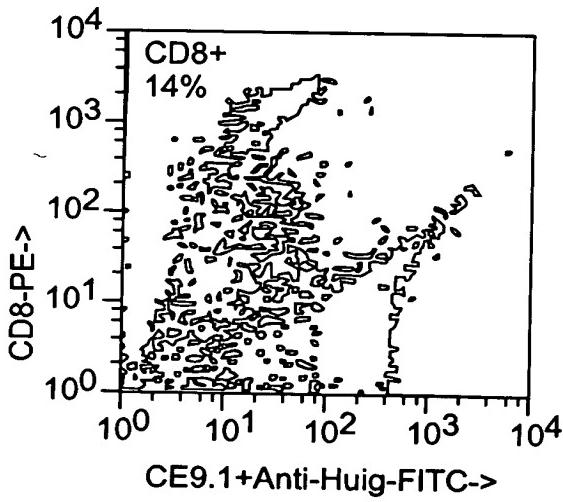
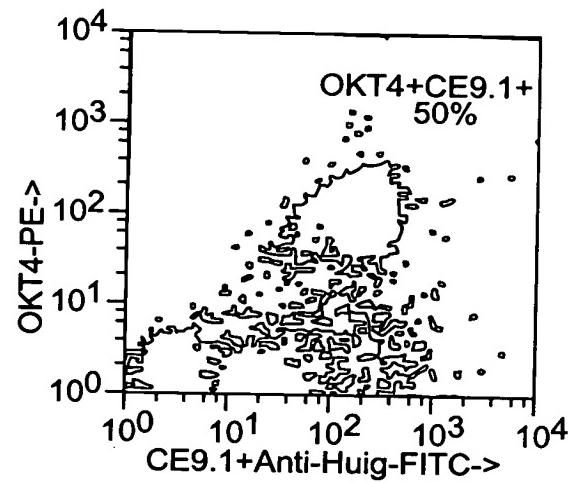
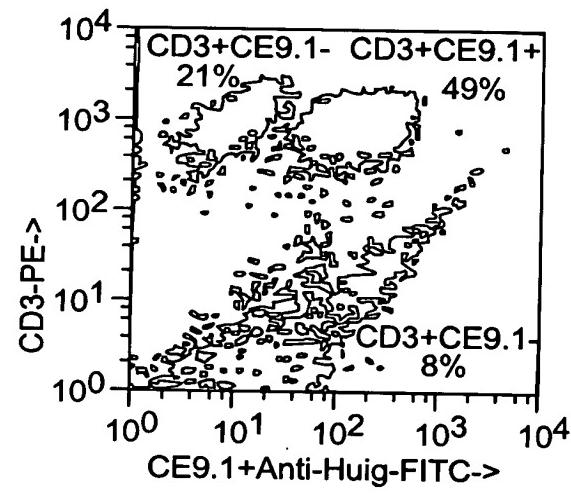


Figure 9

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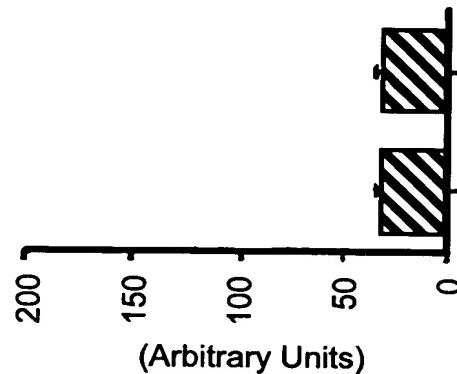


Figure 10c

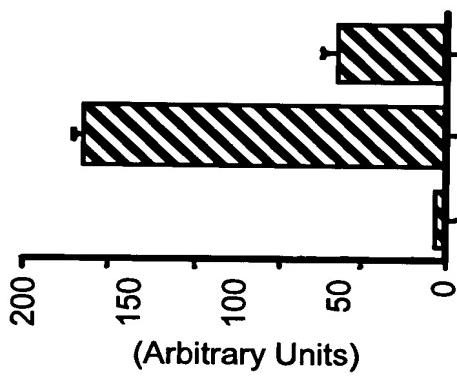


Figure 10b

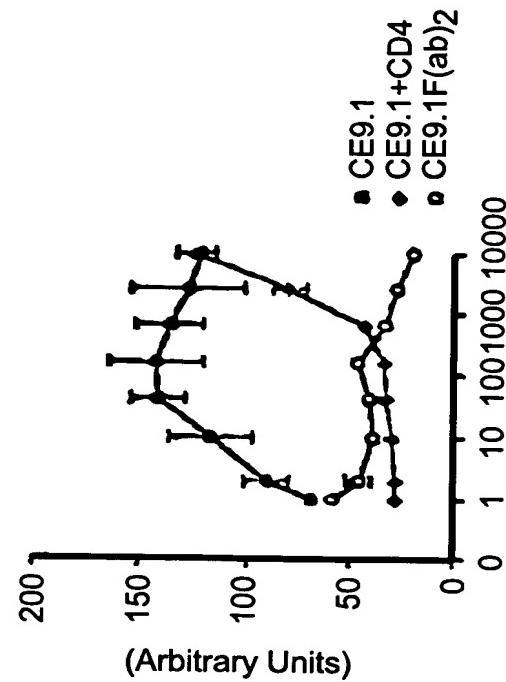


Figure 10a

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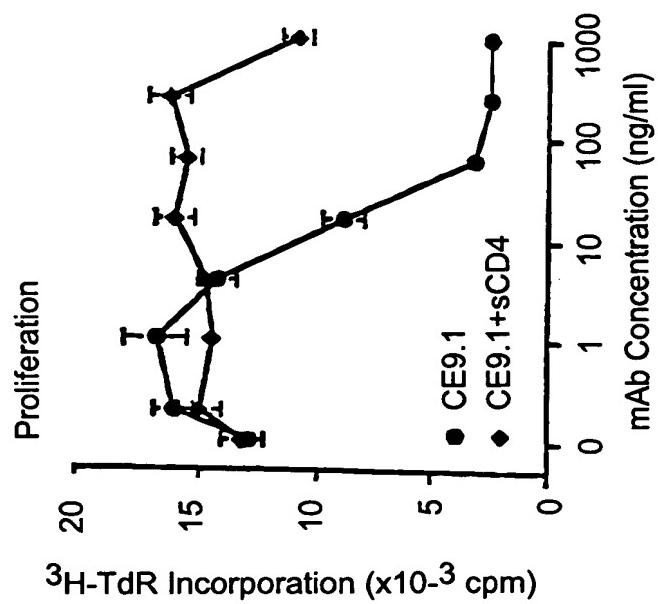
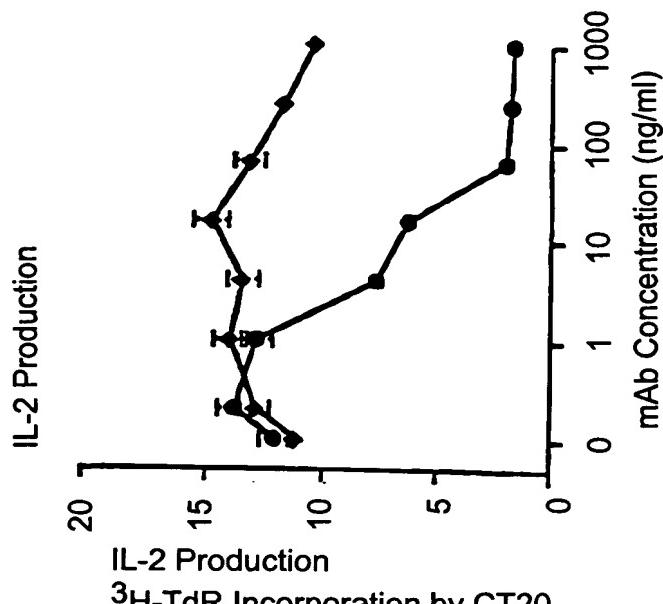


Figure 11



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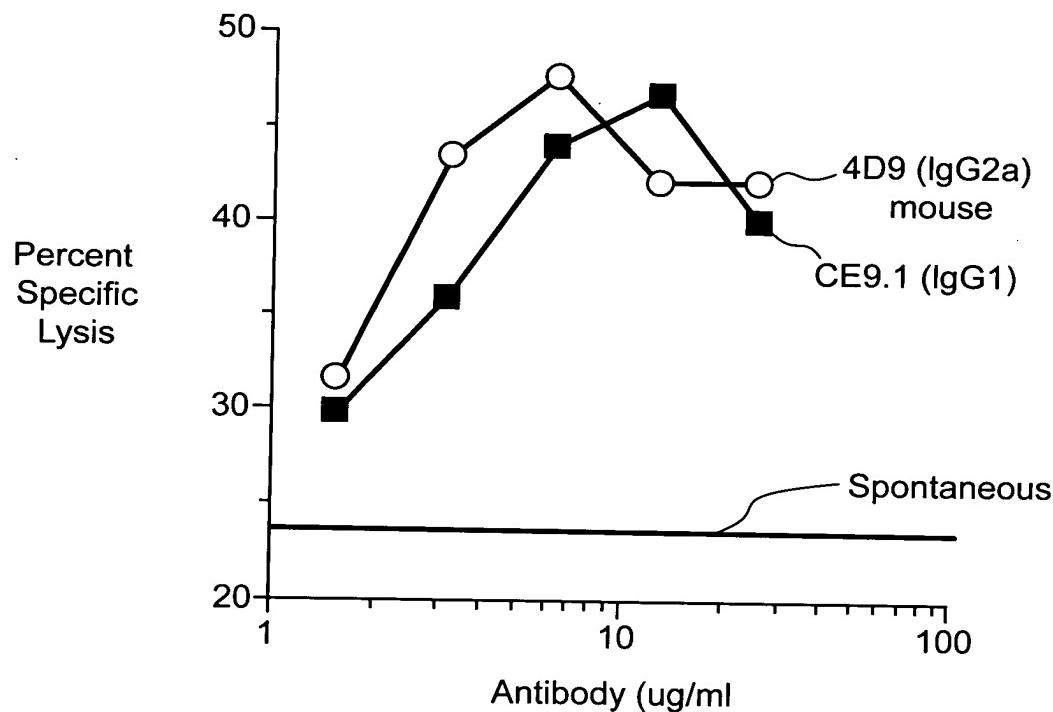


Figure 12

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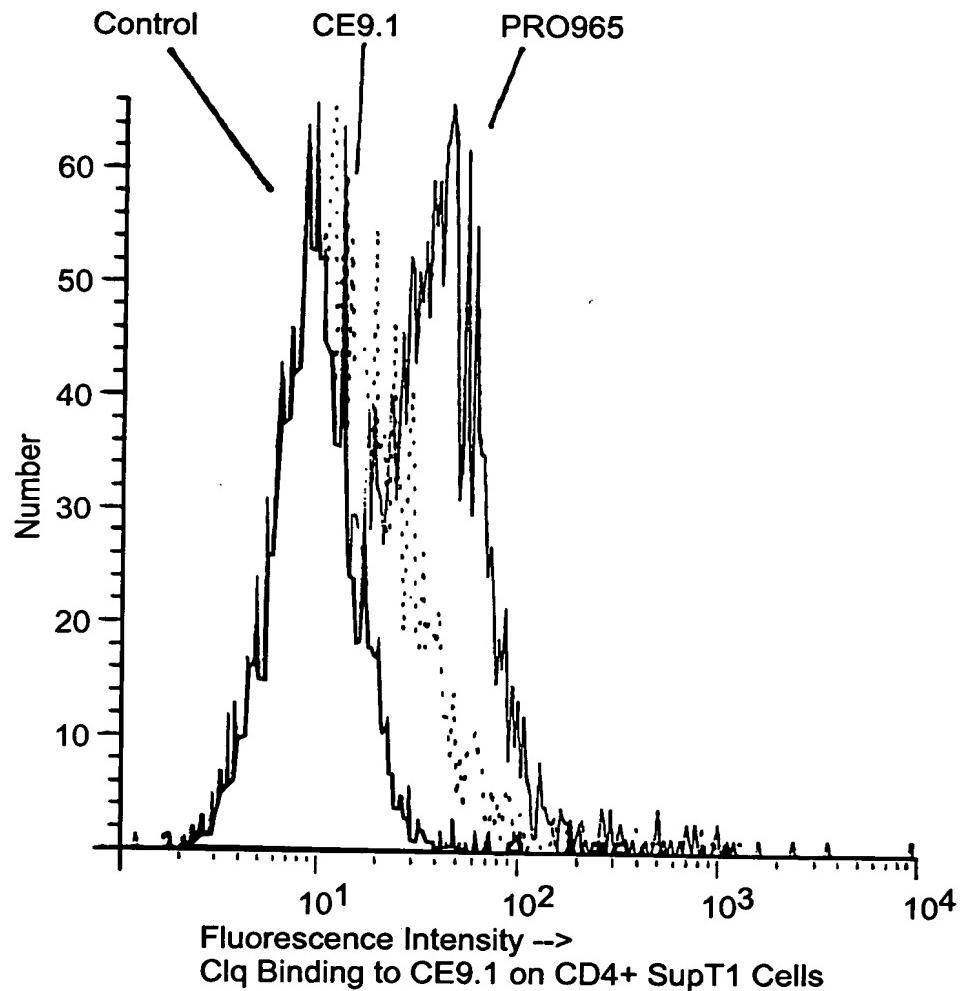


Figure 13



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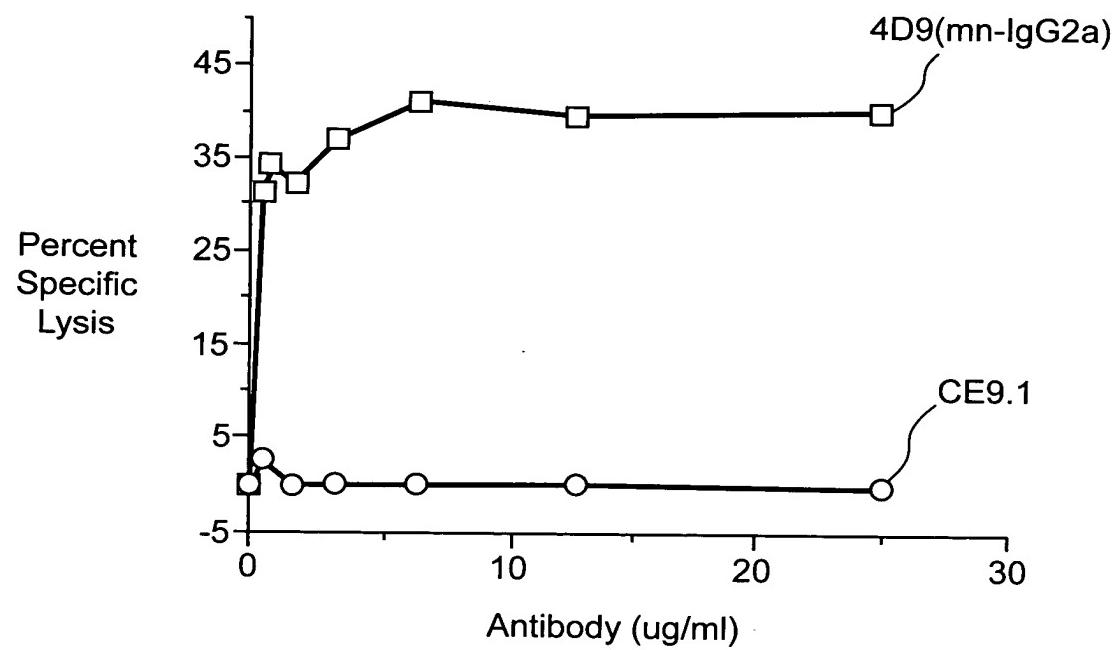


Figure 14



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CD4 and CD8 Cell Counts in Chimpanzees Repeatedly Treated with 10 mpk of CE9.1

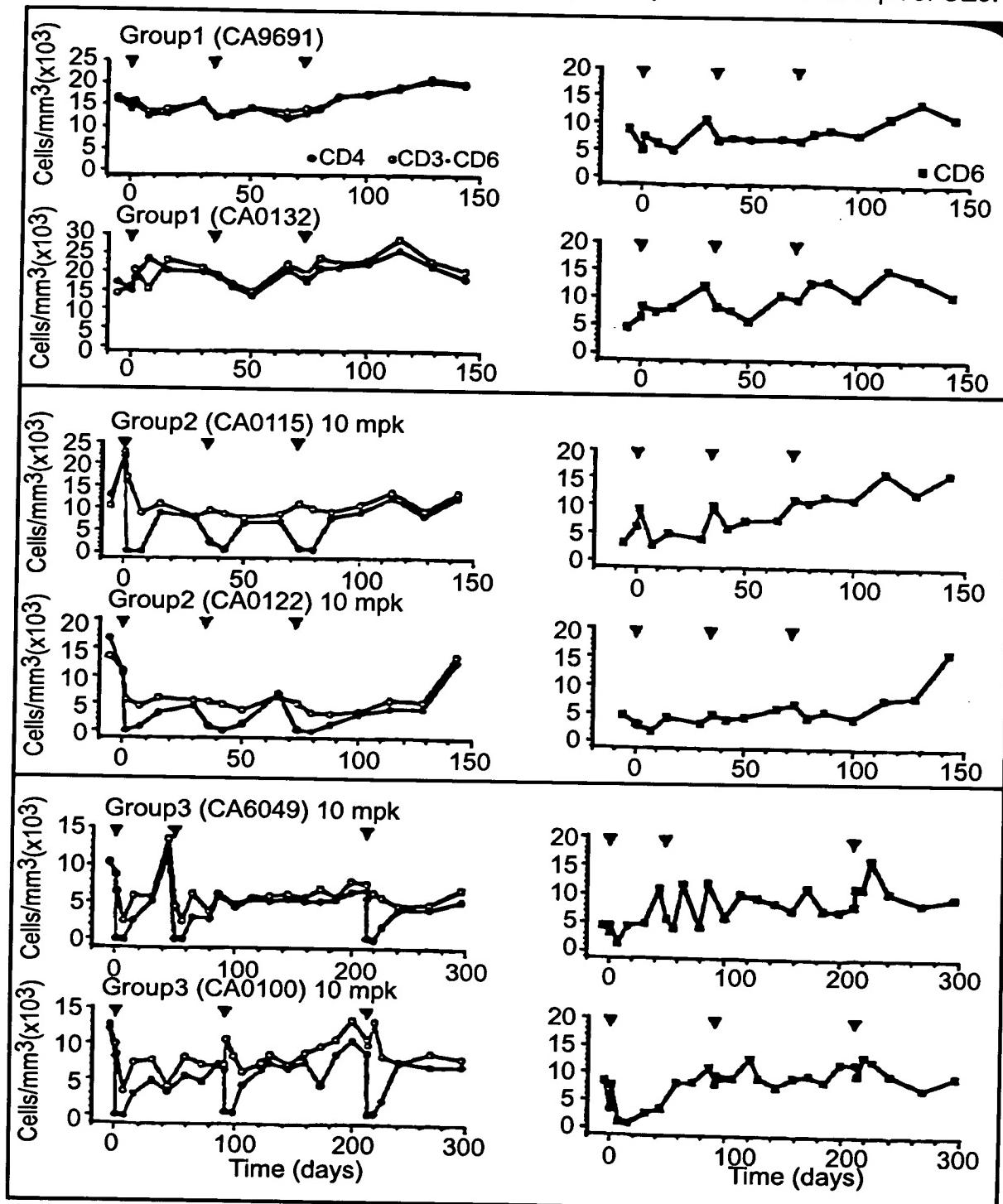


Figure 15



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Figure 16

PCR Primers for Human  $\mu$  Constant Region

1) IDEC 462 3' PCR Primer

5' GGGG GGA TCC TCA TTT ACC CAG AGA CAG GG 3'  
BamH I  
Nhe I

2) IDEC 479 5' PCR Primer

5' GGGG GCT ACC AAG GGC CCA TCC GTC TTC 3'  
Nhe I

PCR Mutagenesis of Human  $\mu$

3) IDEC 698 3' PCR Primer

5' CCG GGA GAT CAT GAG AGT GTC CTT GGG TTT TGG GGG GAA CAG GAA GAC  
BspH I  
Glu

4) Midland GE2112 5' PCR Primer

5' TCC TCA GCT AGC ACC AAG GGG CCA TCC TGG GCA TGG GGG 3'  
Nhe I  
Destroys Apa I site



Appn. No.: 09/612,814  
INVENTOR: Nabil HANNA et al.  
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## Figure 17a

Frame 1 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser  
ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCC CCC AGA TGG GTC TTG TCC  
9 18 27 36 45 54

+1  
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr  
CAG GTG CAG CTG CAG GAG TCG GGC CCA GGA CTG GTG AAG CCT TCG GAG ACC CTG TCC CTC ACC  
66 75 84 93 102 111 120

Cys Ser Val Ser Gly Gly Ser Ile Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro  
TGC AGT GTC TCT GGT GGC TCC ATC AGC GGT GAC TAT TAT TGG TTC TGG ATC CGC CAG TCC CCA  
129 138 147 156 165 174 183

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser GLY Gly Gly Thr Asn Tyr Asn Pro  
GGG AAG GGA CTG GAG TGG ATC GGC TAC ATC TAT GGC AGT GGT GGG GGC ACC AAT TAC AAT CCC  
192 201 210 219 228 237 246

Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys Asn Leu Phe Ser Leu Lys Leu  
TCC CTC AAC AAT CGA GTC TCC ATT TCA ATA GAC ACG TCC AAG AAC CTC TTC TCC CTG AAA CTG  
255 264 273 282 291 300 309

Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu  
AGG TCT GTG ACC GCC GCG GAC ACG GCC GTC TAT TAC TGT GCG AGT AAT ATA TTG AAA TAT CTT  
318 327 336 345 354 363 372

His Trp Leu Leu Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
CAC TGG TTA TTA TAC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC TCA GCT AGC ACC AAG GGG  
381 390 399 408 417 426 435



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**Figure 17b**

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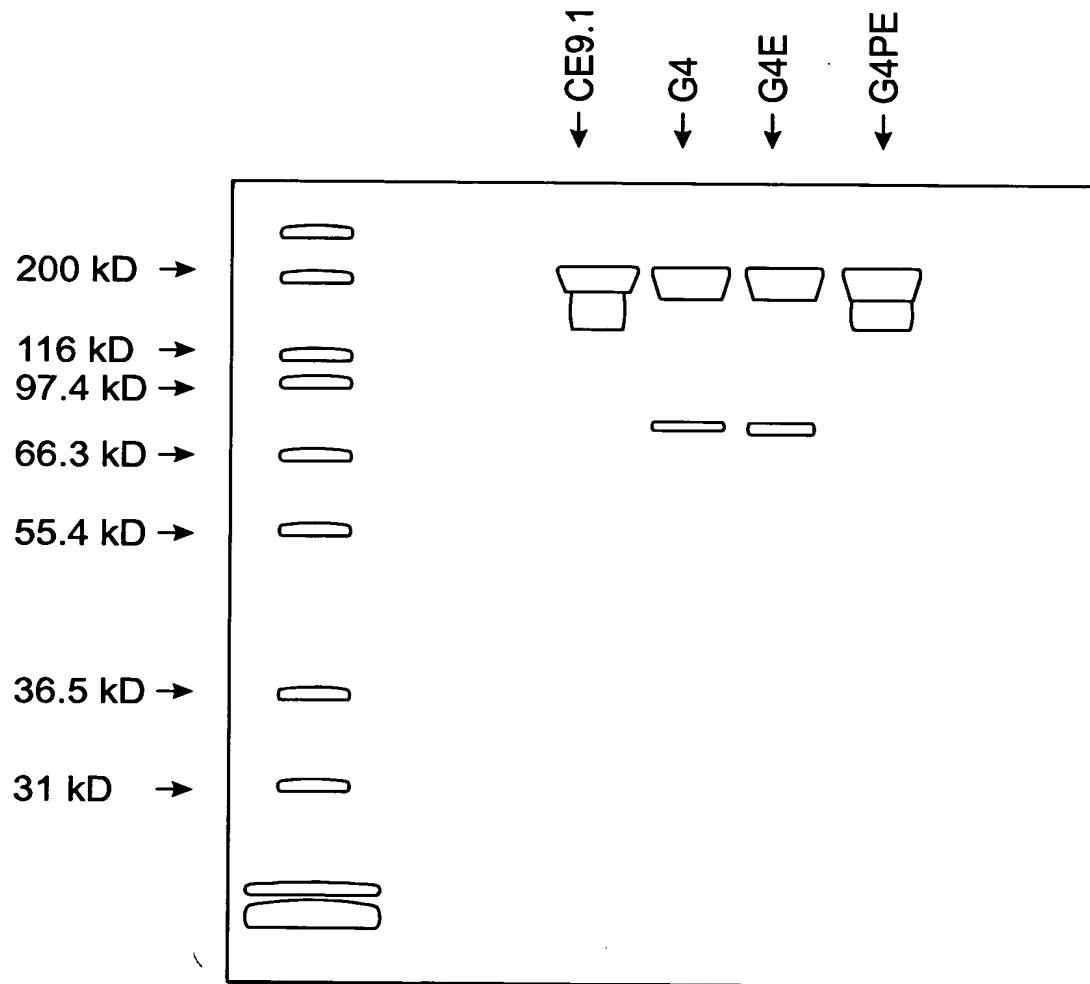


Figure 18

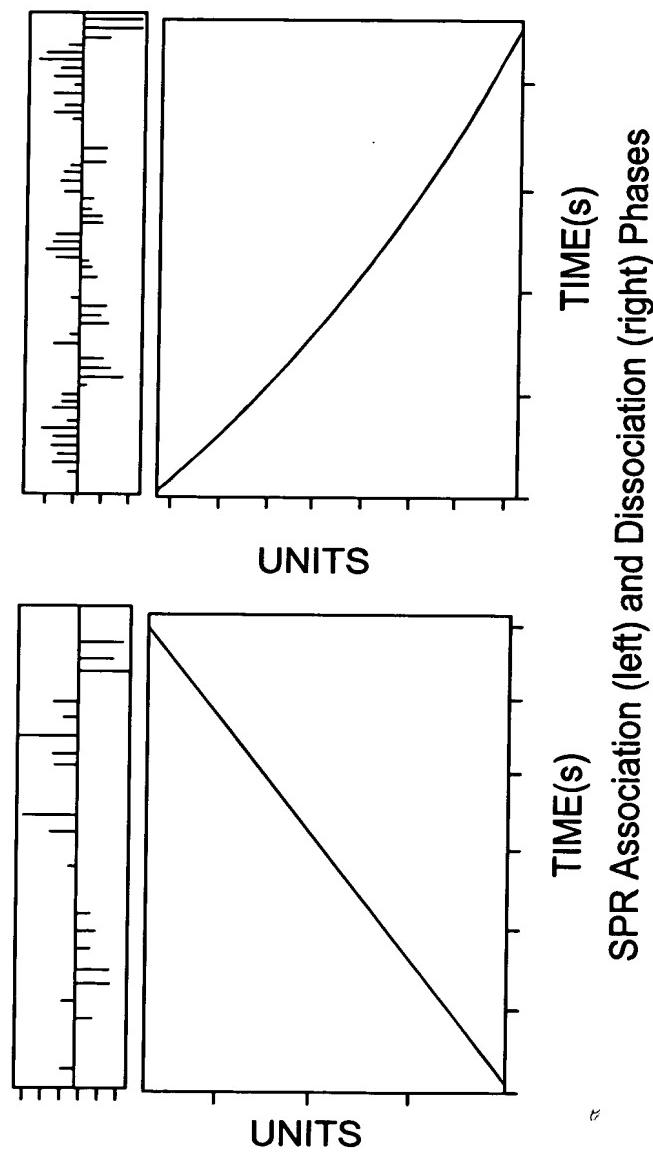
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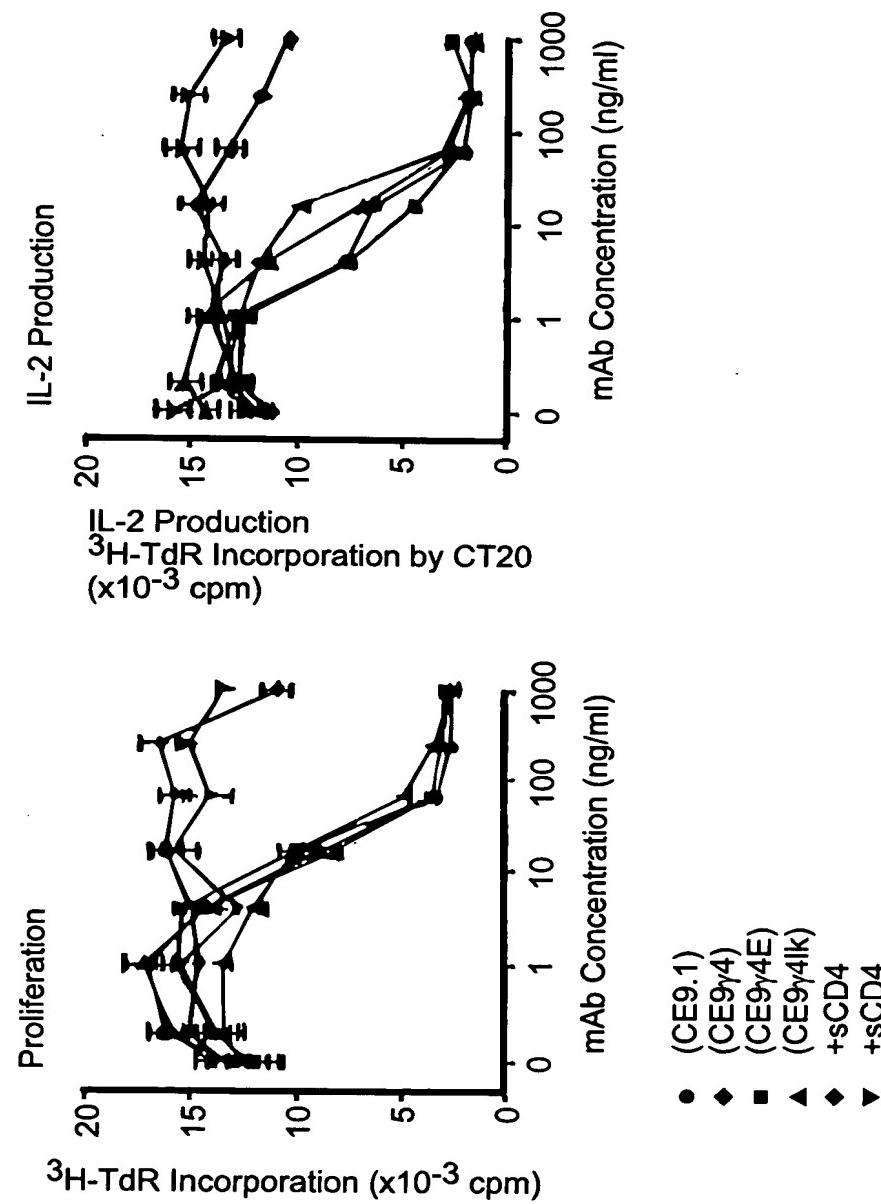
Figure 19



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Figure 20



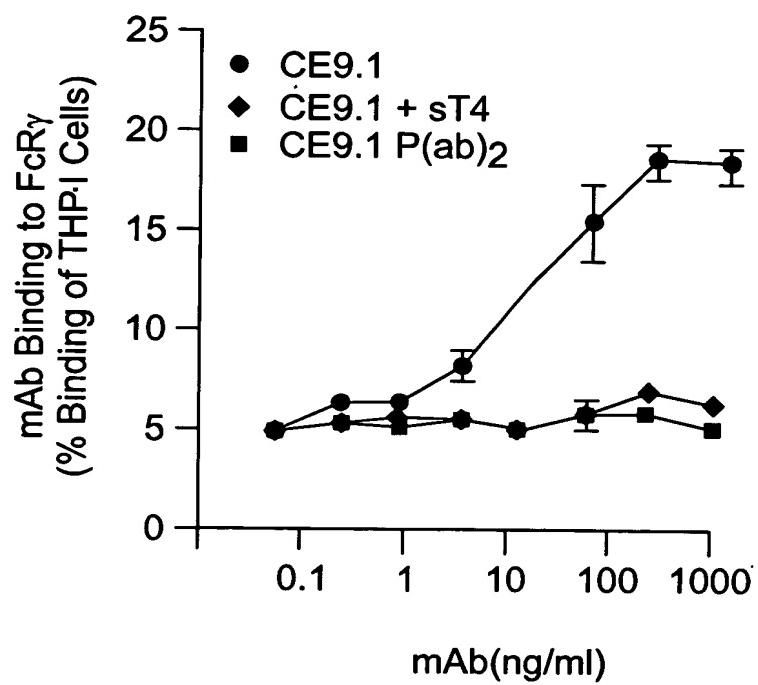


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Figure 21



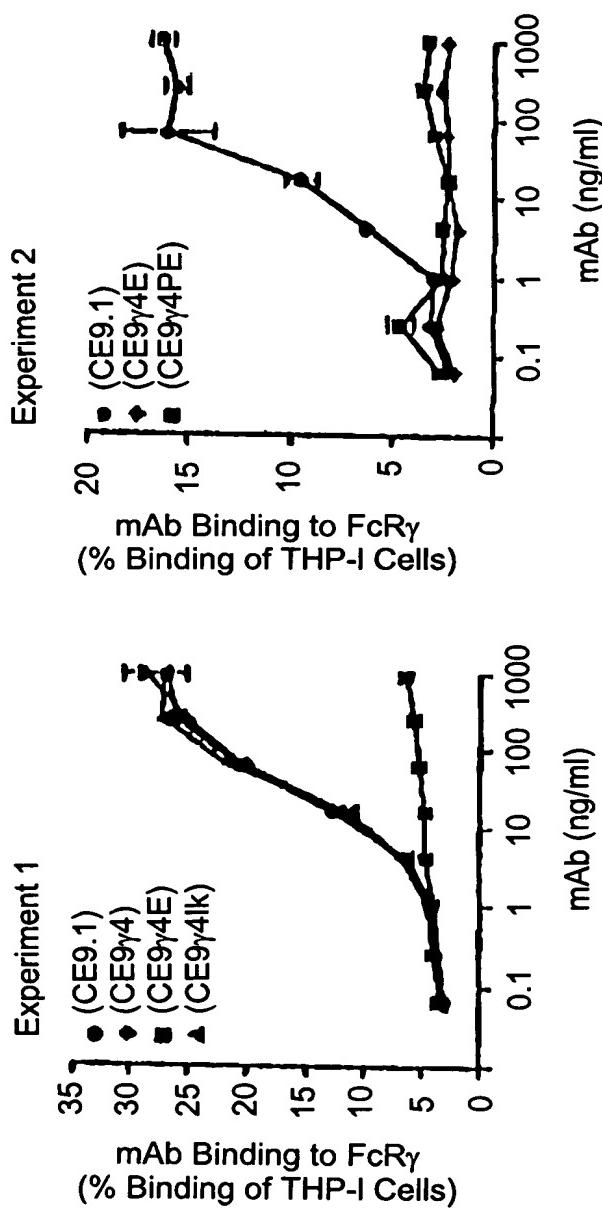
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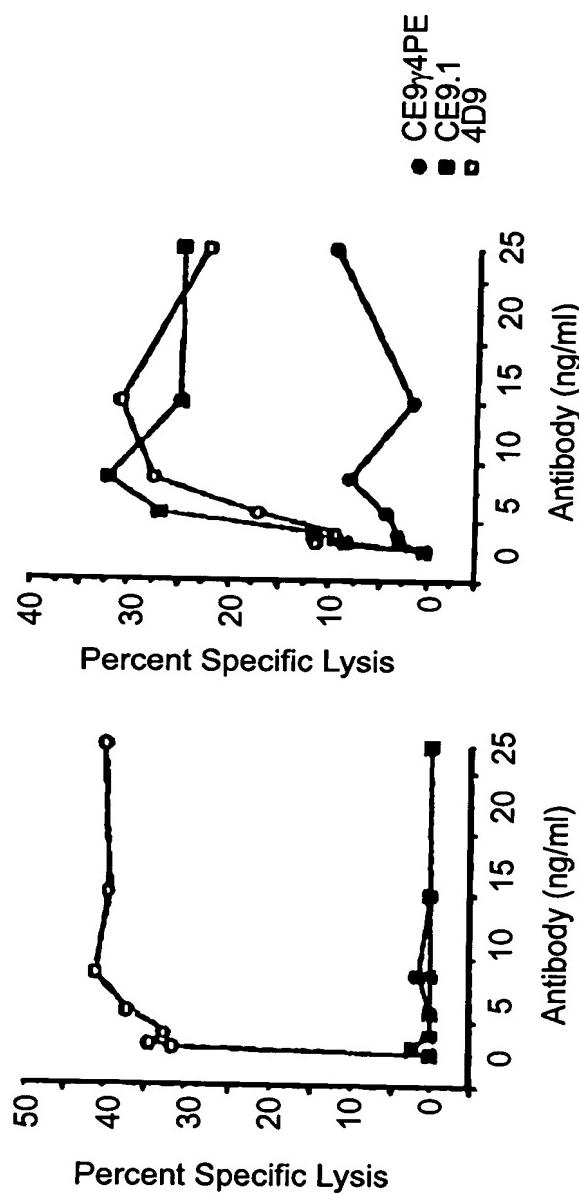


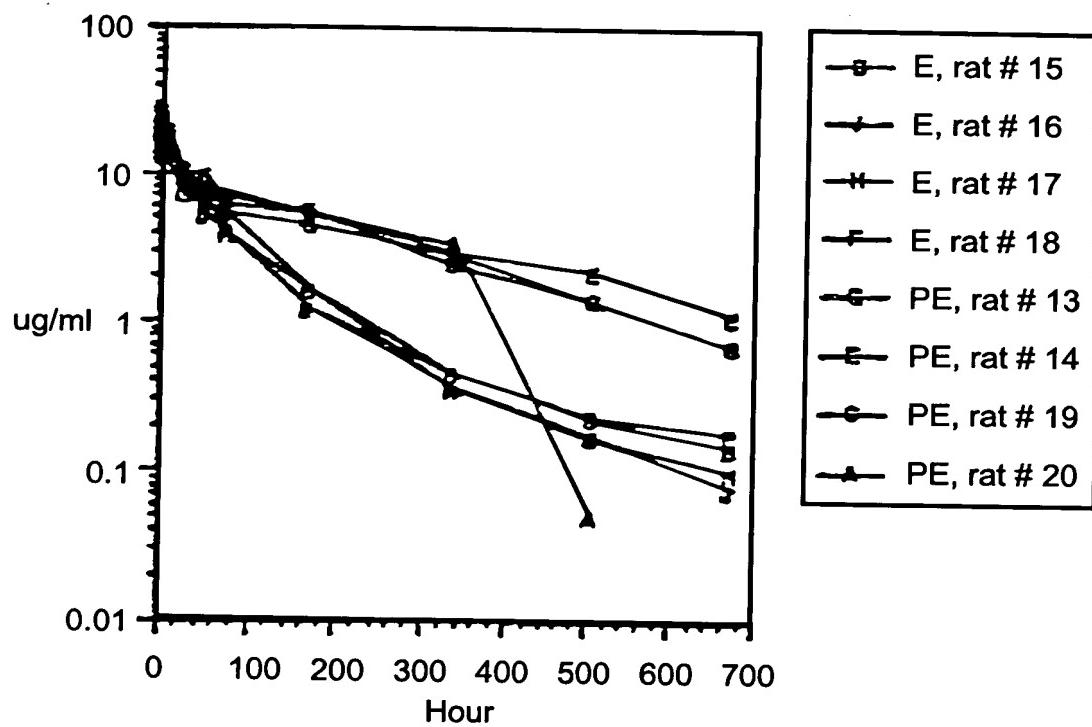
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Figure 24





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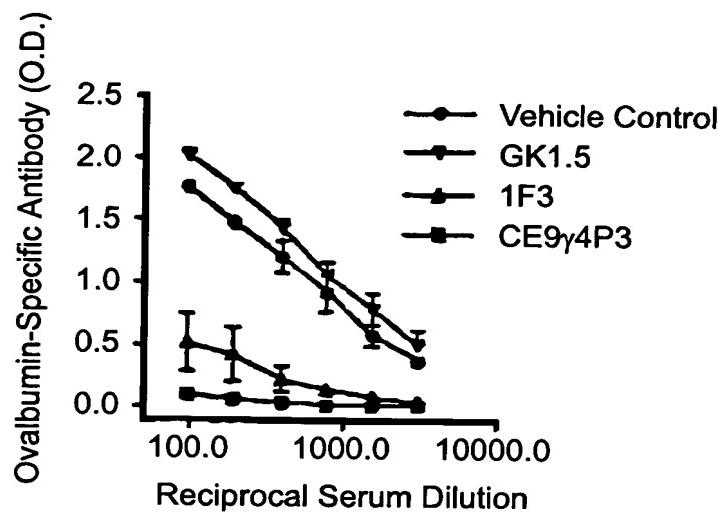


Figure 25